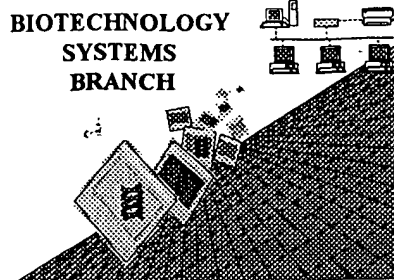# RAW SEQUENCE LISTING
# ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: _09/895,913_

Source: _OIPE_

Date Processed by STIC: _7/23/2001_

**THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.**
**PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:**
1) **INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,**
2) **TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY**
**FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.**

**FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.**
**PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)**
**PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)**

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE **CHECKER VERSION 3.0 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

## Checker Version 3.0

The Checker Version 3.0 application is a state-of the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.
Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:
http://www.uspto.gov/web/offices/pac/checker

OIPE

RAW SEQUENCE LISTING               DATE: 07/23/2001
PATENT APPLICATION:  US/09/895,913     TIME: 13:44:58

Input Set : A:\06132.013001.seqlist.txt
Output Set: N:\CRF3\07232001\I895913.raw

**Does Not Comply**
**Corrected Diskette Needed**

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  4 <110> APPLICANT: Kleanthous, Harold
  5         Al-Garawi, Amal
  6         Miller, Charles
  7         Tomb, Jean Francois
  8         Oomen, Raymond P.
 10 <120> TITLE OF INVENTION: IDENTIFICATION OF POLYNUCLEOTIDES
 11         ENCODING NOVEL HELICOBACTER POLYPEPTIDES IN THE HELICOBACTER
 12         GENOME
 14 <130> FILE REFERENCE: 06132/043001
 16 <140> CURRENT APPLICATION NUMBER: US/09/895,913
 17 <141> CURRENT FILING DATE: 2001-06-29
 19 <160> NUMBER OF SEQ ID NOS: 368
 21 <170> SOFTWARE: FastSEQ for Windows Version 3.0
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ERRORED SEQUENCES

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1161 <210> SEQ ID NO: 12
1162 <211> LENGTH: 1844                    pp 4-6
1163 <212> TYPE: PRT
1164 <213> ORGANISM: Helicobacter pylori
1166 <400> SEQUENCE: 12
1167   Leu Leu Gly Thr Met Met Met Met Leu Phe Gln Gln Asn Leu Trp Trp
1168   1               5                   10                  15
1169   Phe Asn Asn Ile Met Val Val Glu Gln Gly Gly Ser Ile Ile Ile Ile
1170                   20                  25                  30
1171   Ile Ser Gly Thr Pro Pro Phe Val Gln Gln His Pro Lys Lys Thr Ala
1172               35                  40                  45
1173   Ala Lys Phe Val Val Val Val Val Glu Glu Glu Phe Ser Ser Ala Leu
1174       50                  55                  60
1175   Ser Ser Tyr Lys Lys Phe His Tyr Tyr Ile Leu Arg Arg Arg Arg Phe
1176   65                  70                  75                  80
1177   Ser Thr Thr Asp Ala Asp Asp Gly Gly Phe Gly Val Val Val Arg Lys
1178               85                  90                  95
1179   Lys Ile His Ser Arg Arg Lys Pro Pro Val Cys Val Val Arg Val Leu
1180               100                 105                 110
1181   Leu Ser Arg Arg Tyr Lys Asn Asn Asn Asn Asn Asp Leu Leu Trp Leu
1182           115                 120                 125
1183   Leu Leu Arg Arg Ser Leu Leu Leu Trp Gly Gly Arg Trp Gly Leu Cys
1184       130                 135                 140
1185   Cys Leu Gly Ser Ser Ser Arg Arg Lys Pro Ile Ile Asn Gly Gly Gly
1186   145                 150                 155                 160
1187   Asp Leu Leu Leu Leu Leu Trp Glu Glu Ile Cys Cys Tyr Leu His His
1188               165                 170                 175
1189   Gln Phe Gln Gln Arg Leu Leu Ile Phe Leu Leu Leu Leu Leu Asn Asn
1190               180                 185                 190
1191   Asn Cys Arg Arg Thr Leu Thr Thr Gly Gly Gly Gly Asp Asp Asp Ile
```

```
1192              195                 200                 205
1193    Leu Thr Thr Thr Thr Leu Met Lys Lys Leu Asn Ala Ala Arg Val Val
1194        210                 215                 220
1195    Ile Thr Arg Arg Phe Gln Thr Thr Gly Phe Phe Phe Phe Phe Leu Thr
1196    225                 230                 235                 240
1197    Asn Asn Val Arg Arg Gln His Ser Ser Gly Glu Phe Phe Ile Pro Pro
1198                    245                 250                 255
1199    Leu Ser Met Met Met Met Met Ile Lys Lys Phe Leu Leu Gly Ile Ser
1200            260                 265                 270
1201    Ser Trp Gly Gly Leu Phe Phe Ile Gln Gly Gly Gly Gly Val Ser Leu
1202            275                 280                 285
1203    Leu Glu Asn Thr Thr Phe Ala Gly Pro Pro Ile Asn Gly Gly Asp Arg
1204        290                 295                 300
1205    Leu Ile Ile Met Met Val Ala Ala Tyr Gly Phe Phe Tyr Phe Phe Asn
1206    305                 310                 315                 320
1207    Ser Ile Ile Ile Ile Ile Gly Gly Gly His Ser Leu Leu Ile Lys Lys
1208                    325                 330                 335
1209    Asn Asn Asn Tyr Phe Gln Gln Thr Leu Lys Lys Lys Lys Trp Leu Leu
1210            340                 345                 350
1211    Leu Val Ser Lys Lys Cys Glu Glu Ser His His His Asn Gly Asn Asn
1212            355                 360                 365
1213    Tyr Phe Phe Phe Phe Phe Phe Gln Gln Phe Gln Gln Lys Pro Asn Asn
1214        370                 375                 380
1215    Gly Tyr Leu Gly Gly Ser Gln Thr Thr Thr Thr Thr Thr Ala Ala Arg
1216    385                 390                 395                 400
1217    Lys Arg Arg Gln Ala Phe Phe Phe Tyr Tyr Gln Gln Arg Arg Arg Ile
1218                . 405                 410                 415
1219    Leu Leu Leu Leu Thr Ala Gln Gln Ala Phe Asn Asn Gly Val Val Ile
1220            420                 425                 430
1221    Ile Ile Asn Pro Asn Asn Ser Ser Ser Ser Ser Ser Leu Gln Ser Ser
1222            435                 440                 445
1223    Ile Ile Asn Asn Ala Ala Cys Asn Phe Phe Met Ala Ala Pro Leu Phe
1224        450                 455                 460
1225    Phe Phe Phe Phe Lys Thr Thr Phe Trp Trp Thr Leu His His Leu Ile
1226    465                 470                 475                 480
1227    Ile Phe Gln Arg Arg Ile Arg Ile Ile Ile Ile Leu Ile Lys Lys Thr
1228                    485                 490                 495
1229    Leu Asn Asn Lys Gly Gly Lys Ile Ser Ser Ile Asn Phe Phe Arg Arg
1230            500                 505                 510
1231    Arg Arg Arg Arg Tyr Phe Lys Thr Thr Thr Met Asn Asn Ser Lys Lys
1232            515                 520                 525
1233    Pro Lys Lys Ser Phe Asn Asn Asn Asn Asn Leu Lys Lys Gly Arg Gly
1234        530                 535                 540
1235    Gly Arg Ile Ser Ser Leu Asn Asn Leu Lys Leu Leu Ile Ser Ser Ser
1236    545                 550                 555                 560
1237    Ser Met Ala Ile Ile Val Phe Asn Asn Ser Cys Cys Val Phe Met Met
1238                    565                 570                 575
1239    Asn His Ser Ser Asn Phe Phe Phe Phe Phe His Ile Ile Arg Leu Leu
1240            580                 585                 590
```

```
1241  Asn Ser Asp Asp Phe Phe Ala Ala Asn Ser Thr Thr Thr Thr Thr Asn
1242          595                 600                 605
1243  Phe Phe Lys Arg Ser Ser Met Val Val Leu Asn Asn Phe Arg Gln Gln
1244      610                 615                 620
1245  Ala Val Thr Thr Thr Thr Ile Arg Arg Asn Ala Lys Lys Glu Phe Phe
1246  625                 630                 635                 640
1247  Val Leu Gly Gly Lys Gly Ile Ile Glu Ser Ser Ser Ser Ser Leu Tyr
1248              645                 650                 655
1249  Glu Glu Tyr Leu Leu Gly Asp Lys Lys Asn Phe Arg Arg Met Met Met
1250          660                 665                 670
1251  Leu Gln Ala Ala Ala Ala Ala Asn Ile Ile Trp Leu Asn Asn Gly Ile
1252          675                 680                 685
1253  Thr Thr Tyr Glu Glu Asp Pro Phe Phe Met Ala Tyr Tyr Tyr Tyr Arg
1254          690                 695                 700
1255  Leu Thr Thr Ala Asp Tyr Tyr Val Thr Ala Phe Phe Ser Trp Arg Arg
1256  705                 710                 715                 720
1257  His Ala Gln Tyr Tyr Leu Lys Lys Ile Thr Glu Glu Leu Ala Thr Ala
1258              725                 730                 735
1259  Ala Lys Val Gln Gln Gln Gln Gln Ser Gln Gln Arg Arg Phe Phe Ile
1260          740                 745                 750
1261  Ile Arg Arg Phe Asn Asn Arg Ser Cys Met Ile Ile Ile Ile Thr Lys
1262          755                 760                 765
1263  Lys Lys Pro Tyr Asn Asn Asn Arg Arg Ile Pro Ile Ile Tyr Thr Ser
1264          770                 775                 780
1265  Ser Gly Gly Gly Gly Gly His Leu Leu Leu Arg Arg Asn Ile Lys Lys
1266  785                 790                 795                 800
1267  Leu Ser Ser Thr Ile Ile Thr Pro Gly Gly Gly Gly Gly Tyr Asn Asn
1268              805                 810                 815
1269  Ala Lys Pro Pro Pro Tyr Lys Lys Leu His His Leu Gln Ser Ser Leu
1270          820                 825                 830
1271  Ser Leu Leu Leu Leu Ser Lys Ile Ile Asn Met Ile Ile Gln Phe Phe
1272          835                 840                 845
1273  Val Arg Ser Ser Leu Pro Lys Lys Ser Gln Gln Gln Gln Gln Phe Ile
1274      850                 855                 860
1275  Phe Phe Gly Leu Leu Asp Asn Leu Leu Pro Glu Glu Val Leu Leu Thr
1276  865                 870                 875                 880
1277  Leu Phe Phe Phe Phe Phe Ile Phe Phe Lys Val Trp Trp Ser Leu Gln
1278              885                 890                 895
1279  Glu Glu Leu Glu Glu Glu Tyr Arg Arg Arg Arg Leu Ser Ile Ile Phe
1280          900                 905                 910
1281  Ser Asn Asn Asn Met Ile Ser Ser Gln Gly Asn Asn Arg Cys Cys Cys
1282          915                 920                 925
1283  Cys Cys Ser Asp Gln Gln Arg Gly Gly Thr Asn Thr Thr Lys Arg Gly
1284      930                 935                 940
1285  Gly Gly Leu Leu Gly Glu Gly Gly Gly Gly Gly Lys Glu Glu Met Cys
1286  945                 950                 955                 960
1287  Gly Gly Gly Ile Thr Thr Cys Gln Gln Val Gln Thr Thr Leu Ile Gly
1288              965                 970                 975
1289  Asn Cys Cys His Ser Ser Ser Ala Leu Leu Ala Thr Thr Asn Ala Asn
```

```
     1290            980              985              990
     1291 Asn Gly Gly Gly Gly Gly Lys His Leu Leu Leu Pro Pro Thr Ile Gly
     1292            995             1000             1005
     1293 Gly Arg Glu Arg Arg Gly Gly Gly Gly Gly Ser Ser Ser Ser Ser Asn
     1294           1010             1015             1020
     1295 Val Val Phe Lys Lys Ala Leu Ile Ile Val Leu Leu Ser Ser Leu Thr
E--> 1296 1025            1030             1035             (104) 1040
     1297 Leu Leu Leu Leu Lys Gly Pro Pro Lys Ile Phe Phe Leu Leu Leu Gly
     1298           1045             1050             1055
     1299 Lys Gly Gly Ile Glu Lys Lys Phe Trp Trp Trp Trp Trp Lys Arg Phe
     1300           1060             1065             1070
     1301 Phe Gly Met Met Leu Ser Asn Asn His Leu Arg Ala Ala Asn Asp Asn
     1302           1075             1080             1085
     1303 Asn Asn Asn Asn Ile Pro Pro Arg Phe Ser Ser Thr Ser Ser Lys Asp
     1304           1090             1095             1100
     1305 Asp Trp Ile Leu Ala Ala Ala Ala His Cys Leu Leu Pro Thr Glu Glu
E--> 1306 1105            1110             1115             (112)
     1307 Glu Ser Ala Ala Ser Ala Phe Phe Lys Arg Arg Arg Arg Arg His Gly
     1308           1125             1130             1135
     1309 Asn Asn Ile Ile Lys Thr Val Val Arg Cys Phe Phe Val Lys Lys Gly
     1310           1140             1145             1150
     1311 Leu Leu Leu Leu Leu Leu Ala Leu Leu Ser Tyr Gly Gly Glu Lys Lys
     1312           1155             1160             1165
     1313 Lys Asp Gln Gln Ala Phe Arg Arg Lys Ser Lys Lys Lys Lys Pro Ile
     1314           1170             1175             1180
     1315 Leu Leu Gly Phe Glu Glu Ile His His Lys Leu Leu Gly Ile Glu Glu
E--> 1316 1185            1190             1195             (120)
     1317 Cys Arg Arg Arg Arg Arg Phe His Gln Gln Thr Gly Gly Gly Lys Gln
     1318           1205             1210             1215
     1319 Gln Leu Glu Phe Phe Leu Pro Pro Asn Phe Val Val Val Val Val Gly
     1320           1220             1225             1230
     1321 Gly Gly Glu Ser Ser Ser Leu Ile Lys Lys Gly Ser Ser Leu Cys Cys
     1322           1235             1240             1245
     1323 Lys Thr Tyr Tyr Tyr Tyr Arg Thr Ser Ser Asp Lys Thr Thr Phe Trp
     1324           1250             1255             1260
     1325 Trp Ile Phe Gln Met Ile Ile Thr Ser Ser Ser Ser Ser Leu Asn Gln
E--> 1326 1265            1270             1275             (128)
     1327 Gln Asn Ser Ser Ser Trp Leu Leu Ser Ala Gly Gly Ala Ala Leu Val
     1328           1285             1290             1295
     1329 Asn Asn Asn Asn Asn Ala Leu Leu His His His Thr Leu Val Val Glu
     1330           1300             1305             1310
     1331 Leu Leu His His His Leu Ala Val Lys Lys Lys Leu Asn Asp Asp Ile
     1332           1315             1320             1325
     1333 Arg Arg Met Ala Asn Lys Ile Ile Glu Gln Gln Gln Gln Gln Ser Leu
     1334           1330             1335             1340
     1335 Arg Arg Lys Asn Lys Ile Ile Cys Ala Leu Leu Gly Val Tyr Tyr Tyr
E--> 1336 1345            1350             1355             (136)
     1337 Tyr Tyr Gln Gly Gly Arg Leu His His Cys Leu Asn Asn Leu Gln Gln
     1338           1365             1370             1375
```

*(handwritten note in right margin)* When numbering the last amino acid on a line, please end the number directly under the last letter of the amino acid e.g. Thr 1040

```
       1339  Ile Glu Glu Asn Trp Ala Ala Ala Ala Trp Ala Leu Leu Leu Gly Ser
       1340            1380            1385            1390
       1341  Ser Gly Val Val Thr Ile Phe Phe Gln Arg Gly Gly Phe Gln Gln Gln
       1342            1395            1400            1405
       1343  Gln Gln Cys Gly Ile Ile Ile Phe Thr Asn Asn Gln Leu Val Val Val
       1344        1410            1415            1420
       1345  Thr Thr Thr Gly Gly Gly Gly Gly Gly Leu Asn Asn Cys Gly Gly Gly
E--> 1346  1425            1430            1435            144
       1347  Ser Leu Leu Leu Phe Asn Asn Glu Lys Tyr Tyr Ser Ile Ser Ser Ser
       1348            1445            1450            1455
       1349  Ser Arg Ser Ile Ile Gly Lys Leu Leu Val Tyr Tyr Leu Lys Ile Ile
       1350            1460            1465            1470
       1351  Ser Asn Ile Ile Ile Arg Arg Arg Arg Arg Leu Lys Arg Arg Leu Thr
       1352            1475            1480            1485
       1353  Thr Leu Thr Leu Leu Cys Ser Met Thr Thr Ser Val Gln Gln Gln Gln
       1354        1490            1495            1500
       1355  Gln Gly Gln Gln Leu Arg Glu Glu Phe Ile Ile Met Gly Gly Glu Lys
E--> 1356  1505            1510            1515            152
       1357  Ser Ser Ile Leu Gln Gln Gln Gln Ala Arg Gln Gln Pro Thr Asn Asn
       1358            1525            1530            1535
       1359  Asn Thr Thr Lys Arg Met Met Asn Asn Phe Phe Phe Phe Phe Phe Phe
       1360            1540            1545            1550
       1361  Phe Cys Asn Leu Met Met Leu Val Asp Asp Phe Lys Ser Ser Tyr Lys
       1362        1555            1560            1565
       1363  Lys Thr Thr Ile Ile Ile Ile Ile Thr Leu Leu Phe Arg Ala Ala Thr
       1364        1570            1575            1580
       1365  Leu Leu Leu Lys Ala Ala Ser Phe Asp Asp Ile Thr Thr Thr Thr Leu
E--> 1366  1585            1590            1595            160
       1367  Leu Thr Thr Asn Ser Asn Asn Gln Gly Gly Ile Leu Ala Ala Asn Leu
       1368            1605            1610            1615
       1369  Asn Asn Gly Ser Gly Ser Ser Ala Arg Arg Glu Asn Gly Gly Glu Cys
       1370            1620            1625            1630
       1371  Gly Gly Ala Ile Ile Lys Ser Glu Glu Glu Glu Glu Ser Leu Leu Leu
       1372        1635            1640            1645
       1373  Ser Ser Thr Ile Lys Lys Asn Gln Gln Asp Tyr Trp Leu Ala Ala Ala
       1374        1650            1655            1660
       1375  Ala Ile Leu Arg Arg Met Ser Tyr Tyr Gln Ser Ser Leu Ser Ser Phe
E--> 1376  1665            1670            1675            168
       1377  Asn Thr Thr Thr Gln Gln Gln Gln Gln Arg Arg Leu Leu Arg Leu Leu
       1378            1685            1690            1695
       1379  Asn Ala Lys Lys His Ala Leu Leu Val Met Met Asn Gln Ile Ile Ile
       1380            1700            1705            1710
       1381  Ile Ile Arg Gly Gly Glu Leu Glu Glu Ile Thr Ser Ser Leu Tyr Tyr
       1382            1715            1720            1725
       1383  Pro His Leu Thr Ala Ala Ala Ala Asn Ala Cys Cys Leu Asn Gly Gly
       1384            1730            1735            1740
       1385  Phe Thr Thr Ala Met Thr Thr Gln Pro Val Val Tyr Trp Gly Ser Ser
E--> 1386  1745            1750            1755            176
       1387  Trp Phe Lys Asp Asp Ser Gly Ala Ala Trp Cys Cys Ser Ser Ile Ile
```

```
     1388                    1765              1770              1775
     1389     Ile Ile Ile Tyr Asp Asp Ser Ser Ser Ser Ala Ser Leu Leu Lys Pro
     1390              1780          1785              1790
    ·1391     Pro Gly Tyr Ser Ser Pro Leu Val Val Val Trp Ser Ile Ile Ile
     1392          1795              1800              1805
     1393     Lys Tyr Tyr Ser Arg Arg Val Leu Val Val Asp Ala Ile Ile Ile Cys
     1394          1810              1815              1820
     1395     Cys Cys Cys Cys Gln Phe Phe Phe Cys Cys Leu Asn Glu Glu Phe Cys
E--> 1396     1825              1830              1835              184
     1397     Gly Gly Lys Gly
     1463     <210> SEQ ID NO: 14
     1464     <211> LENGTH: 189
     1465     <212> TYPE: PRT
     1466     <213> ORGANISM: Helicobacter pylori
     1468     <400> SEQUENCE: 14
     1469     Met Ile Asn Arg Ala Thr Leu His Asn Tyr Ser Glu Ile Glu Lys Lys
     1470     1             5                 10              15
     1471     Asn Ile Met Leu Ser Asp Arg Val Val Val Ile Arg Ser Gly Asp Val
     1472              20                25              30
     1473     Ile Pro Lys Ile Ile Lys Pro Leu Glu Ser Tyr Arg Asp Gly Ser Gln
     1474              35                40                45
     1475     His Lys Ile Glu Arg Pro Lys Val Cys Pro Ile Cys Ser His Glu Leu
     1476          50                55                60
     1477     Leu Cys Glu Glu Ile Phe Thr Tyr Cys Gln Asn Leu Asn Cys Pro Ala
     1478     65                70                75                80
     1479     Arg Leu Lys Glu Ser Leu Ile His Phe Ala Ser Lys Asp Ala Leu Asn
     1480              85                90                95
     1481     Ile Gln Gly Leu Gly Asp Lys Val Ile Glu Gln Leu Phe Glu Glu Lys
     1482              100               105               110
     1483     Leu Ile Phe Asn Ala Leu Asp Leu Tyr Ala Leu Lys Leu Glu Asp Leu
     1484              115               120               125
     1485     Met Arg Leu Asp Lys Phe Lys Ile Lys Lys Ala Gln Asn Leu Leu Asp
     1486          130               135               140
     1487     Ala Ile Leu Lys Ser Lys Asn Pro Pro Leu Trp Arg Leu Ile Asn Ala
     1488     145               150               155               160
     1489     Leu Gly Ile Glu His Ile Gly Lys Gly Ala Ser Lys Thr Leu Ala Lys
     1490              165               170               175
E--> 1491     Tyr Gly Leu Asn Val Leu Glu Lys Ser Glu Xaa Ser Phe
     1492              180               185
     2771     <210> SEQ ID NO: 34
     2772     <211> LENGTH: 454
     2773     <212> TYPE: PRT
     2774     <213> ORGANISM: Helicobacter pylori
     2776     <400> SEQUENCE: 34
     2777     Met Phe Leu Leu Arg His Leu Thr Ser Ala Cys Val Phe Leu Ala Ser
     2778     1             5                 10              15
     2779     Lys Cys Leu Pro Asp Ser Phe Val Leu Val Ala Leu Leu Ser Phe Val
     2780              20                25              30
     2781     Val Phe Val Leu Val Tyr Cys Leu Thr Gly Gln Asp Ala Phe Ser Val
```

```
2782            35                  40                  45
2783  Ile Ser Ser Trp Gly Asn Gly Ala Trp Thr Leu Leu Gly Phe Ser Met
2784      50                  55                  60
2785  Gln Met Ala Leu Ile Leu Val Leu Gly Gln Ala Leu Ala Asn Ala Lys
2786  65                  70                  75                  80
2787  Leu Val Gln Lys Leu Leu Lys Tyr Leu Ala Ser Leu Pro Lys Gly Tyr
2788                  85                  90                  95
2789  Tyr Thr Ala Leu Trp Leu Val Thr Phe Leu Ser Leu Ile Ala Asn Trp
2790                  100                 105                 110
2791  Ile Asn Trp Gly Phe Gly Leu Val Ile Ser Ala Ile Phe Ala Lys Glu
2792                  115                 120                 125
2793  Ile Ala Lys Asn Val Lys Gly Val Asp Tyr Arg Leu Leu Ile Ala Ser
2794      130                 135                 140
2795  Ala Tyr Ser Gly Phe Val Ile Trp His Gly Gly Leu Ser Gly Ser Ile
2796  145                 150                 155                 160
2797  Pro Leu Ser Val Ala Thr Gln Asn Glu Asn Leu Ser Lys Ile Ser Ala
2798                  165                 170                 175
2799  Gly Val Ile Glu Lys Ala Ile Pro Ile Ser Gln Thr Ile Phe Ser Ser
2800                  180                 185                 190
2801  Tyr Asn Leu Ile Ile Ile Gly Ile Ile Leu Val Gly Leu Pro Phe Leu
2802                  195                 200                 205
2803  Met Ala Met Ile His Pro Lys Lys Glu Glu Ile Val Glu Ile Asp Ser
2804      210                 215                 220
2805  Lys Leu Leu Lys Asp Glu Tyr Lys Glu Ile Glu Leu Ile Ser His Gln
2806  225                 230                 235                 240
2807  Gln Asp Lys Thr Ile Ala His Phe Leu Glu Asn Ser Ala Leu Leu Ser
2808                  245                 250                 255
2809  Tyr Leu Leu Val Phe Leu Gly Phe Gly Tyr Leu Gly Val Tyr Phe Phe
2810                  260                 265                 270
2811  Lys Gly Gly Gly Ile Ser Leu Asn Ile Val Asn Thr Ile Phe Leu Phe
2812                  275                 280                 285
2813  Leu Gly Ile Leu Leu His Lys Thr Pro Leu Ala Tyr Val Lys Ala Ile
2814      290                 295                 300
2815  Asp Arg Ser Ala Xaa Ser Val Ala Gly Ile Leu Leu Gln Phe Pro Phe
2816  305                 310                 315                 320
2817  Tyr Ala Gly Ile Met Gly Met Met Ala Ser His Ser Val Gly Gly His
2818                  325                 330                 335
2819  Ser Leu Ala Gln Met Leu Ser Leu Ala Phe Thr His Ile Ala Asn Glu
2820                  340                 345                 350
2821  Lys Thr Phe Val Leu Met Thr Phe Leu Ser Ala Gly Ile Val Asn Ile
2822                  355                 360                 365
2823  Phe Ile Pro Ser Gly Gly Gly Gln Trp Ala Ile Gln Ala Pro Ile Met
2824      370                 375                 380
2825  Leu Pro Ala Gly Gln Ser Leu Gly Val Asp Pro Gly Val Val Ser Met
2826  385                 390                 395                 400
2827  Ala Ile Ala Trp Gly Asp Ala Trp Thr Asn Met Ile Gln Pro Phe Trp
2828                  405                 410                 415
2829  Ala Leu Pro Ala Leu Ala Ile Ala Gly Leu Gly Ala Lys Asp Ile Met
2830                  420                 425                 430
```

E--> 2815 (circled: Xaa at position ~307)

see item 9

Input Set : A:\06132.013001.seqlist.txt
Output Set: N:\CRF3\07232001\I895913.raw

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2831  Gly Tyr Cys Val Leu Thr Leu Ile Phe Val Gly Leu Val Val Cys Gly
2832          435                 440                 445
2833  Val Phe Tyr Phe Leu Val
2834      450
9641  <210> SEQ ID NO: 146
9642  <211> LENGTH: 435
9643  <212> TYPE: PRT
9644  <213> ORGANISM: Helicobacter pylori
9646  <400> SEQUENCE: 146
9647  Met Gly Phe Phe Lys Leu Lys Glu His Asn Thr Asn Ile Ala Thr Glu
9648  1               5                   10                  15
9649  Phe Arg Ala Gly Leu Thr Thr Phe Ile Thr Met Ile Tyr Ile Val Pro
9650          20                  25                  30
9651  Leu Asn Ala Leu Ile Leu Ser Gln Ala Asn Met Pro Tyr Glu Ala Leu
9652          35                  40                  45
9653  Leu Ser Ala Thr Ala Ile Ile Thr Ile Leu Ser Ser Val Phe Asn Gly
9654      50                  55                  60
9655  Leu Trp Ala Asn Thr Pro Ile Ala Met Ser Val Gly Leu Gly Leu Ser
9656  65                  70                  75                  80
9657  Ala Tyr Phe Ser Phe Gly Leu Val Gln Gly Leu Lys Leu Pro Trp Gln
9658              85                  90                  95
9659  Ser Ala Leu Gly Ile Val Ala Leu Ser Gly Ala Ile Phe Val Ile Leu
9660              100                 105                 110
9661  Ser Phe Thr Lys Phe Arg Ser Trp Val Met Arg Ser Ile Pro Ser Asp
9662              115                 120                 125
9663  Leu Arg Arg Ala Val Ser Ala Gly Ile Gly Ala Phe Ile Ala Phe Ile
9664          130                 135                 146
9665  Gly Leu Lys Glu Met His Ile Val Val Thr His Xaa Ala Thr Leu Val
9666  145                 150                 155                 160
9667  Thr Leu Gly Asp Phe Gly Asp Pro His Val Leu Leu Gly Val Val Gly
9668              165                 170                 175
9669  Ile Ile Leu Thr Phe Ala Leu Tyr Thr Leu Lys Ile Arg Gly Ser Phe
9670              180                 185                 190
9671  Ile Ile Ala Val Leu Ile Thr Ser Ile Leu Ala Trp Val Leu Lys Leu
9672          195                 200                 205
9673  Ala Pro Tyr Pro Ser Glu Phe Phe Ser Met Pro Ala Ser Ile Gly Pro
9674      210                 215                 220
9675  Ile Ala Phe Gln Leu Asp Phe Lys Gly Ile Phe Phe Asp Ala Ser Gly
9676  225                 230                 235                 240
9677  Ala Phe Thr Leu Ala Leu Val Pro Val Ile Ile Thr Phe Phe Val Thr
9678              245                 250                 255
9679  Asp Leu Phe Asp Ser Leu Gly Thr Leu Ala Gly Ile Gly His Lys Thr
9680              260                 265                 270
9681  Asp Phe Phe Asn Asp Glu Glu Lys Asn Lys Glu Leu Glu Lys Thr Leu
9682          275                 280                 285
9683  Glu Ala Asp Ala Val Ala Ser Leu Gly Ser Ala Val Val Gly Val Ser
9684      290                 295                 300
9685  Thr Thr Thr Ala Phe Ile Glu Ser Ala Ser Gly Val Glu Glu Gly Gly
9686  305                 310                 315                 320
```

E--> 9665 (line, left margin)

(handwritten, right margin) see item 9

```
9687   Arg Thr Gly Leu Thr Ala Val Phe Thr Gly Leu Phe Phe Val Leu Thr
9688               325             330             335
9689   Leu Phe Cys Leu Pro Leu Leu Lys Ala Ile Pro Ser Asn Ala Ile Tyr
9690               340             345             350
9691   Pro Val Leu Val Val Val Gly Val Leu Met Phe Ser Val Leu Glu Gly
9692               355             360             365
9693   Val Asn Phe Lys Asp Met Ala Ile Ser Val Ser Thr Phe Leu Thr Val
9694         370             375             380
9695   Val Met Met Pro Leu Thr Phe Ser Ile Ala Asp Gly Leu Ala Phe Gly
9696   385             390             395             400
9697   Phe Leu Ser Tyr Ser Ile Ile Lys Leu Val Gln Lys Asp Phe Lys Ala
9698               405             410             415
9699   Leu Asn Ser Gly Ile Ile Ile Leu Cys Ile Ile Ser Val Ser Val Phe
9700               420             425             430
9701   Ile Phe Arg
9702               435
16782  <210> SEQ ID NO: 246
16783  <211> LENGTH: 1185
16784  <212> TYPE: PRT
16785  <213> ORGANISM: Helicobacter pylori
16787  <400> SEQUENCE: 246
16788  Met Gln Lys Ile Ile Asp Asp Ser Leu Glu Leu Ala Lys Lys Leu Gln
16789    1               5              10              15
16790  Asp Ser Ile Ser Asn His Leu Ser Asp Gln Glu Lys Ala Phe His Ser
16791               20              25              30
16792  Lys Met Gln Lys Leu Leu Asn Asn Pro Glu Asn Lys Val Met Leu Ile
16793               35              40              45
16794  Glu Leu Met Asp Arg Ser Phe Arg Cys Leu Asp Asn Lys Ala Arg Phe
16795         50              55              60
16796  Glu Met Ile Glu His Val Leu Asp Lys Tyr Lys Ser Arg Glu Ile Phe
16797   65              70              75              80
16798  Ser Pro Phe Glu Lys Val Leu Leu Met Gly Phe Leu Ser Phe Gly Lys
16799               85              90              95
16800  Met Leu Pro Asp Met Ser Val Pro Phe Phe Val Asn Lys Ile Arg Ser
16801               100             105             110
16802  Asp Thr Lys Ala Met Val Leu Asp Gln Glu Glu Ser Gln Leu Lys Glu
16803               115             120             125
16804  Arg Ile Leu Lys Arg Lys Asn Glu Lys Ile Ile Leu Asn Val Asn Phe
16805         130             135             140
16806  Ile Gly Glu Glu Val Leu Gly Glu Glu Glu Ala Asn Ala Arg Phe Glu
16807   145             150             155             160
16808  Lys Tyr Ser Gln Ala Leu Lys Ser Asn Tyr Ile Gln Tyr Ile Ser Ile
16809               165             170             175
16810  Lys Ile Thr Thr Ile Phe Ser Gln Ile Asn Ile Leu Asp Phe Glu Tyr
16811               180             185             190
16812  Ser Lys Lys Glu Ile Val Lys Arg Leu Asp Ala Leu Tyr Ala Leu Ala
16813               195             200             205
16814  Leu Glu Glu Glu Lys Lys Gln Gly Met Pro Lys Phe Ile Asn Leu Asp
16815         210             215             220
```

```
16816   Met Glu Glu Phe Arg Asp Leu Glu Leu Thr Val Glu Ser Phe Met Glu
16817   225                 230             235                 240
16818   Ser Ile Ala Lys Phe Asp Leu Asn Ala Gly Ile Val Leu Gln Ala Tyr
16819               245                 250                 255
16820   Ile Pro Asp Ser Tyr Glu Tyr Leu Lys Lys Leu His Ala Phe Ser Lys
16821               260                 265                 270
16822   Glu Arg Val Leu Lys Gly Leu Lys Pro Ile Lys Ile Arg Phe Val Lys
16823           275                 280                 285
16824   Gly Ala Asn Met Glu Ser Glu Glu Thr Ile Ala Ser Val Lys Asp Trp
16825       290                 295                 300
16826   Ala Leu Pro Thr Phe Ser Asn Lys Gln Asp Thr Asp Ser Asn Tyr Asn
16827   305                 310                 315                 320
16828   Lys Met Leu Asp Phe Val Leu Glu Gly Asp Asn Tyr Lys Tyr Ile His
16829               325                 330                 335
16830   Ile Gly Ala Ala Ser His Asn Ile Phe Glu Ile Ala Tyr Val Tyr Thr
16831               340                 345                 350
16832   Arg Ile His Ala Ile Asn Asp Pro Val Val Leu Glu His Phe Ser Phe
16833           355                 360                 365
16834   Glu Met Leu Glu Gly Met Ser Leu Gln Ala Ser Gln Glu Leu Lys Glu
16835       370                 375                 380
16836   Met His Lys Leu Ile Leu Tyr Ala Pro Val Cys Asp Glu Ala His Phe
16837   385                 390                 395                 400
16838   Asn Asn Ala Ile Ala Tyr Leu Val Arg Arg Leu Asp Glu Asn Thr Ser
16839               405                 410                 415
16840   Ser Asp Asn Phe Met Lys Ala Phe Phe Asn Leu Lys Val Gly Thr Ser
16841               420                 425                 430
16842   Glu Trp Lys Asp Gln Glu Gln Arg Phe Leu Asn Ser Leu Lys Gly Ile
16843           435                 440                 445
16844   Ala Thr Leu Asp Asn Ala Thr His Arg Thr Gln Asp Arg Asn Ala Lys
16845       450                 455                 460
16846   Gln Ser Gly His Thr Thr Tyr Pro Asn His Ser Phe Lys Asn Glu Ser
16847   465                 470                 475                 480
16848   Asp Thr Asp Phe Ile Leu Lys Ala Asn Arg Glu Trp Ala Lys Lys Val
16849               485                 490                 495
16850   Arg Glu Lys Met Arg Asn Ala Pro Ile Leu Glu Leu Tyr Pro Glu Met
16851               500                 505                 510
16852   Asp Gly Arg Phe Glu Asp Pro Asn Leu Thr Pro Leu Glu Val Phe Asp
16853           515                 520                 525
16854   Arg Ile His His Lys Lys Ile Ala Ser Val His Leu Ala Asp Lys Glu
16855       530                 535                 540
16856   Ala Ile Leu Lys Ala Leu Glu Val Ala Lys Ser Asp Lys Ser Arg Phe
16857   545                 550                 555                 560
16858   Ser Gln Lys Ser Phe Thr Glu Ile His Ala Leu Met Ser Gln Thr Ala
16859               565                 570                 575
16860   Gln Leu Phe Arg Glu Arg Arg Gly Asp Leu Ile Gly Ile Ser Ala Leu
16861               580                 585                 590
16862   Glu Val Gly Lys Thr Phe Ala Glu Thr Asp Ala Glu Val Ser Glu Ala
16863           595                 600                 605
16864   Ile Asp Phe Leu Glu Phe Tyr Pro Tyr Ser Leu Arg Val Leu Gln Glu
```

```
16865        610                   615                   620
16866   Gln Asn Thr Lys Thr Gln Phe Thr Pro Lys Gly Val Gly Val Val Ile
16867   625                   630                   635                   640
16868   Ala Pro Trp Asn Phe Pro Val Gly Ile Ser Val Gly Thr Ile Ala Ala
16869                   645                   650                   655
16870   Pro Leu Ala Thr Gly Asn Arg Val Ile Tyr Lys Pro Ser Ser Leu Ser
16871                   660                   665                   670
16872   Ser Val Thr Gly Tyr Lys Leu Cys Glu Cys Phe Trp Asp Ala Gly Val
16873               675                   680                   685
16874   Pro Arg Asp Ala Leu Ile Tyr Leu Pro Ser Lys Gly Ser Asp Ile Ser
16875           690                   695                   700
16876   Glu His Leu Leu Arg Asp Glu Ser Ile Gln Phe Ala Ile Leu Thr Gly
16877   705                   710                   715                   720
16878   Gly Glu Asp Thr Ala Tyr Lys Met Leu Lys Ala Asn Pro Thr Leu Ala
16879                   725                   730                   735
16880   Leu Ser Ala Glu Thr Gly Gly Lys Asn Ala Thr Ile Val Ser Lys Met
16881                   740                   745                   750
16882   Ala Asp Arg Asp Gln Ala Ile Lys Asn Val Ile His Ser Ala Phe Ser
16883               755                   760                   765
16884   Asn Ser Gly Gln Lys Cys Ser Ala Thr Ser Leu Leu Val Leu Glu Lys
16885           770                   775                   780
16886   Glu Val Tyr Glu Asp Glu Asn Phe Lys Lys Thr Leu Ile Asp Ala Thr
16887   785                   790                   795                   800
16888   Leu Ser Leu Ser Val Gly Asp Pro Phe Asp Phe Lys Asn Lys Ile Gly
16889                   805                   810                   815
16890   Ala Leu Ala Asp Lys Pro Asn Glu Lys Val Ile Lys Ala Ile Asp Glu
16891               820                   825                   830
16892   Leu Lys Ser Tyr Glu Asn Tyr Glu Ile Pro Val Ser Phe Val Asn Asp
16893           835                   840                   845
16894   Asn Pro Tyr Leu Met Lys Pro Ser Ile Lys Tyr Gly Thr Lys Lys Gly
16895           850                   855                   860
16896   Asp Phe Thr His Gln Thr Glu Leu Phe Thr Pro Ile Leu Ser Val Met
16897   865                   870                   875                   880
16898   Glu Ala Lys Asp Leu Asp Glu Ala Ile Glu Ile Ala Asn Ser Thr Gly
16899               885                   890                   895
16900   Tyr Gly Leu Thr Ser Ala Leu Glu Ser Leu Asp Glu Arg Glu Trp Glu
16901               900                   905                   910
16902   Tyr Tyr Leu Glu Arg Ile Glu Ala Gly Asn Ile Tyr Ile Asn Lys Pro
16903           915                   920                   925
16904   Thr Thr Gly Ala Ile Val Leu Arg Gln Pro Phe Gly Gly Val Lys Lys
16905           930                   935                   940
16906   Ser Ala Val Gly Phe Gly Arg Lys Val Gly Ile Phe Asn Tyr Ile Thr
16907   945                   950                   955                   960
16908   Gln Phe Val Asn Ile Cys Gln Glu Glu Glu Asp Glu Asn Ala Leu Lys
16909               965                   970                   975
16910   Asn Pro Leu Ser Glu Ala Leu Glu Asn Leu Thr Gln Lys Gly Tyr Asp
16911               980                   985                   990
16912   Glu His Thr His Glu Leu Lys Arg Ala Ile Phe Met Ala Lys Ser Tyr
16913               995                   1000                  1005
```

RAW SEQUENCE LISTING                    DATE: 07/23/2001
PATENT APPLICATION:  US/09/895,913      TIME: 13:45:02

Input Set : A:\06132.013001.seqlist.txt
Output Set: N:\CRF3\07232001\I895913.raw

```
        16914  Ala Tyr His Tyr Lys His Glu Phe Ser Gln Thr Lys Asp Tyr Val Lys
        16915       1010            1015             1020
        16916  Ile Arg Gly Glu Asp Asn Leu Phe Ser Tyr Thr Lys Val Lys Ser Val
E-->    16917  1025            1030            1035            (104)
        16918  Gly Tyr Arg Ile Thr Glu Lys Asp Thr Leu Ser Asp Met Leu Gly Val
        16919           1045            1050            1055
        16920  Ala Leu Ala Cys Leu Ile Ser Gln Ile Pro Leu Thr Leu Ser Ile Glu
        16921           1060            1065            1070
        16922  Asn Glu Arg Thr Asn Lys Asp Leu Thr Phe Phe Leu Glu Cys Leu Lys
        16923           1075            1080            1085
        16924  Ala Leu Gln Ala Ser Ala Pro Ile Val Tyr Glu Ser Leu Gln Lys Phe
        16925           1090            1095            1100
        16926  Ser Glu Lys Leu Asn Thr Phe Asn Arg Val Arg Tyr Leu Lys Ser Asp
E-->    16927  1105            1110            1115            (112)
        16928  Leu Asp Leu Leu His Glu Gln Ala Ser Ala Leu Gly Met Val Leu Ala
        16929           1125            1130            ·1135
        16930  Thr Ala Lys Pro Cys Leu Asn Gly Arg Phe Glu Leu Leu Tyr Tyr His
        16931           1140            1145            1150
        16932  Leu Glu Arg Ser Val Ser Ile Ser Tyr His Arg Tyr Gly Asn Leu Gly
        16933        ·  1155            1160            1165
        16934  Ser Arg Val Leu Arg Gln Pro Thr Cys His Lys Ser Cys Cys Ala Glu
        16935           1170            1175            1180
        16936  Lys
        16937  1185
        21547  <210> SEQ ID NO: 318
        21548  <211> LENGTH: 291
        21549  <212> TYPE: PRT
        21550  <213> ORGANISM: Helicobacter pylori
        21552  <400> SEQUENCE: 318
        21553  Lys Asn Arg Arg Arg Asn Arg Gly Asp Ala Ser Gly Thr Gly Leu Asp
        21554  1               5               10              15
E-->    21555  Lys Leu Ile Asp Ala (Xaa) Pro Leu Arg Phe Phe Asp Val Ala Ile Ala
        21556           20              25              30
        21557  Glu Gln His Ala Leu Thr Ser Ser Ser Ala Met Ala Lys Glu Gly Phe
        21558           35              40              45
        21559  Lys Pro Phe Val Ser Ile Tyr Ser Thr Phe Leu Gln Arg Ala Tyr Asp
        21560           50              55              60
        21561  Ser Ile Val His Asp Ala Cys Ile Ser Ser Leu Pro Ile Lys Leu Ala
        21562  65              70              75              80
        21563  Ile Asp Arg Ala Gly Ile Val Gly Glu Asp Gly Glu Thr His Gln Gly
        21564           85              90              95
        21565  Leu Leu Asp Val Ser Tyr Leu Arg Ser Ile Pro Asn Met Val Ile Phe
        21566           100             105             110
        21567  Ala Pro Arg Asp Asn Glu Thr Leu Lys Asn Ala Val Arg Phe Ala Asn
        21568           115             120             125
        21569  Glu His Asp Ser Ser Pro Cys Ala Phe Arg Tyr Pro Arg Gly Ser Phe
        21570           130             135             140
        21571  Ala Leu Lys Glu Gly Val Phe Glu Pro Ser Gly Phe Val Leu Gly Gln
        21572  145             150             155             160
```

RAW SEQUENCE LISTING      DATE: 07/23/2001
PATENT APPLICATION: US/09/895,913   TIME: 13:45:03

Input Set : A:\06132.013001.seqlist.txt
Output Set: N:\CRF3\07232001\I895913.raw

```
21573   Ser Glu Leu Leu Lys Lys Glu Gly Glu Ile Leu Leu Ile Gly Tyr Gly
21574                   165                 170                 175
21575   Asn Gly Val Gly Arg Ala His Leu Val Gln Leu Ala Leu Lys Glu Lys
21576               180                 185                 190
21577   Asn Ile Glu Cys Ala Leu Leu Asp Leu Arg Phe Leu Lys Pro Leu Asp
21578               195                 200                 205
21579   Pro Asn Leu Ser Ala Ile Val Ala Pro Tyr Gln Lys Leu Tyr Val Phe
21580           210                 215                 220
21581   Ser Asp Asn Tyr Lys Leu Gly Gly Val Ala Ser Ala Ile Leu Glu Phe
21582   225                 230                 235                 240
21583   Leu Ser Glu Gln Asn Ile Leu Lys Pro Val Lys Ser Phe Glu Ile Ile
21584               245                 250                 255
21585   Asp Glu Phe Ile Met His Gly Asn Thr Ala Leu Val Glu Lys Ser Leu
21586               260                 265                 270
21587   Gly Leu Asp Thr Glu Ser Leu Thr Asp Ala Ile Leu Lys Asp Leu Gly
21588           275                 280                 285
21589   Gln Glu Arg
21590           290
24908   <210> SEQ ID NO: 362
24909   <211> LENGTH: 226
24910   <212> TYPE: PRT
24911   <213> ORGANISM: Helicobacter pylori
24913   <400> SEQUENCE: 362
24914   Met Gln Phe Thr Gly Lys Asn Val Leu Ile Thr Gly Ala Ser Lys Gly
24915   1               5                   10                  15
24916   Ile Gly Ala Glu Ile Ala Lys Thr Leu Ala Ser Met Gly Leu Lys Val
24917               20                  25                  30
24918   Trp Ile Asn Tyr Arg Ser Asn Ala Glu Val Ala Asp Ala Leu Lys Asn
24919               35                  40                  45
24920   Glu Leu Glu Glu Lys Gly Tyr Lys Ala Ala Val Ile Lys Phe Asp Ala
24921           50                  55                  60
24922   Ala Ser Glu Ser Asp Phe Ile Glu Ala Ile Gln Thr Ile Val Gln Ser
24923   65                  70                  75                  80
24924   Asp Gly Gly Leu Ser Tyr Leu Val Asn Asn Ala Gly Val Val Arg Asp
24925               85                  90                  95
24926   Lys Leu Ala Ile Lys Met Lys Thr Glu Asp Phe His His Val Ile Asp
24927               100                 105                 110
24928   Asn Asn Leu Thr Ser Ala Phe Ile Gly Cys Arg Glu Ala Leu Lys Val
24929               115                 120                 125
24930   Met Ser Lys Ser Arg Phe Gly Ser Val Val Asn Val Ala Ser Ile Ile
24931           130                 135                 140
24932   Gly Glu Arg Gly Asn Met Gly Gln Thr Asn Tyr Ser Ala Ser Lys Gly
24933   145                 150                 155                 160
24934   Gly Met Ile Ala Met Ser Lys Ser Phe Ala Tyr Glu Gly Ala Leu Arg
24935               165                 170                 175
24936   Asn Ile Arg Phe Asn Ser Val Thr Pro Gly Phe Ile Glu Thr Asp Met
24937               180                 185                 190
24938   Asn Ala Asn Leu Lys Asp Glu Leu Lys Ala Asp Tyr Val Lys Asn Ile
24939               195                 200                 205
```

*p. 14*

```
E--> 24940  Pro Leu Asn Arg Leu Gly Ser Ala Lys Glu Val Ala Glu Ala Val Xaa    item 9
     24941      210             215         220
     24942  Phe Phe
     24943  225
```

Use of n and/or Xaa has been detected in the Sequence Listing. Review the Sequence Listing to insure a corresponding explanation is presented in the <220> to <223> fields of each sequence using n or Xaa.

**VERIFICATION SUMMARY**                    DATE: 07/23/2001
PATENT APPLICATION:  **US/09/895,913**      TIME: 13:45:05

Input Set : **A:\06132.013001.seqlist.txt**
Output Set: **N:\CRF3\07232001\I895913.raw**

L:16 M:270 C: Current Application Number differs, Replaced Current Application Number
L:17 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:1296 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:12
M:332 Repeated in SeqNo=12
L:1457 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:13
L:1457 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13
L:1491 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:14
L:2729 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:33
L:2729 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:33
L:2730 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:33
L:2730 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:33
L:2815 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:34
L:3105 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:41
L:3105 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:41
L:4186 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:59
L:4186 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:59
L:5447 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:85
L:5447 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:85
L:9567 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:145
L:9567 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:145
L:9665 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:146
L:16738 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:245
L:16758 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:245
L:16778 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:245
L:16917 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:246
M:332 Repeated in SeqNo=246
L:21079 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:307
L:21079 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:307
L:21476 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:317
L:21476 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:317
L:21477 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:317
L:21477 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:317
L:21555 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:318
L:24902 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:361
L:24902 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:361
L:24903 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:361
L:24903 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:361
L:24940 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:362